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SW/P103239GB

2. Patent application number (The Patent Office will fill in this part)

0317988.4

3 1 JUL 2003

3. Full name, address and postcode of the or of each applicant (underline all surnames)

Professor Jo Milner Department of Biology University of York YORK Y01 5DD

Patents ADP number (if you know it)

If the applicant is a corporate body, give the country/state of its incorporation

8590531001

01AUG03 E826955-1 002973.

4. Title of the invention

SPLICING VARIANTS

5. Name of your agent (if you have one)

"Address for service" in the United Kingdom to which all correspondence should be sent (including the postcode)

Harrison Goddard Foote

Quality House Quality Court Chancery Lane LONDON, WC2A 1HT GB

Patents ADP number (if you know it)

8238845001

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Country

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	Description	9			
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	Priority documents				
	Translations of priority documents				
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I/We request the grant of a patent on the basis of this application.

Signature

Date

Harrison Godden Foote

31 July 2003

Name and daytime telephone number of person to contact in the United Kingdom

Siobhan Ward

0207 242 2047

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SPLICING VARIANTS

Field of the invention

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This invention relates to abnormal spliced variants of genes implicated in the inhibition of apoptosis and to the regulation of apoptosis through the targeting of such variants.

Background to the invention

Bcl-2 is an inhibitor of apoptosis. The functions of the Bcl-2 protein include protection against mitochondrial changes associated with apoptosis. This is achieved by inhibiting pro-apoptotic proteins and by preventing mitochondrial permeability transition. Apoptosis can be triggered by release of cytochrome c and other pro-apoptotic components fom the mitochondria: Bcl-2 is believed to inhibit such events. Consistent with these functions the Bcl-2 protein is predominantly localised to the mitochondria. Bcl-2 may also have additional anti-apoptotic functions yet to be described. It may also block mitochondrial-independent pathways involved in apoptosis.

The human Bcl-2 gene encodes mRNA transcripts of (i) 720 nucleotides in length for Bcl-2 α and (ii) of 618 nucleotides in length for Bcl-2 β (see Figure 1). Bcl-2 α and Bcl-2 β represent normal, alternatively spliced variants of the same Bcl-2 gene.

Abnormal and/or constitutive expression of functional Bcl-2 can protect mammalian cells from undergoing apoptosis. Such an effect favours continued cell survival and proliferation, and can initiate and/or maintain abnormal and/or cancerous growth.

In colorectal cancer cells evidence for a novel Bcl-2 – p53 axis has been reported for a number of established human colorectal carcinoma cells lines, including the LoVo and SW48 cell lines. Co-pending patent application GB0306148.8 relates to the silencing of Bcl-2 by RNA interference. p53-dependent apoptosis is induced indicating that Bcl-2 constitutively suppresses a pro-apoptotic function of p53 in colorectal cancer cells. Importantly, this pro-apoptotic function of p53 does not require activation of the p53 protein by genotoxic stress or by other means.

There is a need to identify cell growth control targets for treating malignancies in humans and other mammalian species.

Statements of the invention

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According to the present invention there is provided a method of regulating apoptosis in a cell, said method comprising targeting an abnormally spliced mRNA or a product thereof.

Preferably the method involves targeting the junctions of mRNA molecules that are abnormally spliced.

Alternatively the method involves targeting a protein product following translation of an abnormally spliced mRNA.

Preferably the method comprises selective silencing of abnormal splice variants of the Bcl-2 gene. The term 'selectively silencing' is used to indicate that the silencing is specific for the target gene and that there is no interference with normal, endogenous gene expression which might be detrimental to normal non-cancerous cells.

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Preferably the method involves the targeting of abnormal splice variants Bcl-2 α -591; Bcl-2 β -489; and Bcl-2 β -420.

More preferably the method involves targeting the mRNA sequence flanking the splice junction between nucleotides 111 and 241 of Bcl-2α-591.

Preferably the method further comprises introducing into a cell containing said gene, an RNA construct having a nucleotide sequence which is homologous to mRNA within said cell wherein said mRNA includes genetic information of the gene element that is abnormally spliced.

RNA interference (RNAi) induces sequence-specific degradation of homologous mRNA and is initiated by the introduction of dsRNA into cells. In mammalian cells RNAi can be achieved using small interfering dsRNAs (siRNAs), preferably up to 30 nucleotides long and more preferably 21-22 nucleotides long.

The term 'homologous' is used to indicate at least 50%, preferably 85%, more preferably 90%, and more preferably 95% and most preferably 100% homology to the reference nucleic acid sequence.

The present invention relates to the discovery of abnormal splice variants of Bcl-2 mRNA in human colorectal carcinoma cells. Sequence alignments are given in Figure 1. The novel splice junctions conserve the normal triplet framing of the spliced mRNA products and the functional BH1, BH2, BH3 and BH4 domains of the Bcl-2 protein are also conserved.

Abnormal alternatively spliced variants of Bcl-2 may function constitutively to suppress apoptosis in human and other mammalian cells, enabling abnormal cell survival and abnormal cell proliferation. The expression of abnormally spliced variants of Bcl-2 may thus represent a key oncogenic event in the development of cancer. The abnormal splice junctions of the Bcl-2 mRNA molecules represent selective targets for intervention via RNA interference or other means. The mRNA sequence at these abnormal splice junctions is not present in the normally spliced Bcl-2 mRNAs.

These abnormal Bcl-2 mRNA transcripts are shorter than the full length 'wild type' Bcl-2 mRNA. In contrast analysis of the genomic Bcl-2 by PCR amplification gives the predicted length for wild type Bcl-2 DNA (Figure 2). This indicates that the shorter abnormal Bcl-2 mRNA transcripts are indeed generated by alternative splicing of RNA, rather than genomic events with loss of DNA coding sequence from the human Bcl-2 gene.

The abnormal alternative spliced variants of Bcl-2 expressed in human colorectal cancer cells retain all known functional domains of the protein (see Figure 1) and are functional in the suppression of apoptosis. Functionality is also evident in colorectal carcinoma cell lines in which Bcl-2 expression appears to comprise solely of the abnormal alternative spliced form(s). In such cells the selective silencing of Bcl-2 expression by RNA interference induces apoptosis (e.g. LoVo cells; Jiang and Milner, 2003; note that normal full length mRNA for Bcl-2α nor for normal full length Bcl-2β mRNA cannot be detected in LoVo, SW48 or in HCT116 cell lines).

Selective silencing of alternatively spliced Bcl-2 expression may be achieved by RNA interference, or by any other 'silencing means' such as small molecules, peptides and/or related molecules which inhibit Bcl-2, either directly or indirectly, and also Bcl-2 derived products including abnormal Bcl-2 splice variants. Anti-sense RNA, shRNA, miRNA and any other RNA and/or DNA based strategies may also be used. Tumour cells other than colorectal cancer cells may similarly be treated.

In one embodiment the present invention provides a nucleotide construct with a nucleotide sequence which is homologous to mRNA transcribed from an abnormally spliced gene.

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Preferably the nucleotide construct comprises dsRNA. Preferably the construct is 30 or less nucleotides long. More preferably the RNA construct is 20 to 30 nucleotides long. Most preferably the RNA construct is 21 to 22 nucleotides long.

In one embodiment the invention provides a nucleotide construct such as anti-sense RNA, shRNA or miRNA as means for silencing the expression of an abnormally spliced gene for use as a medicament.

In an alternate embodiment the invention provides a small molecule or protein which interacts with or binds with a protein expressed by an abnormally spliced mRNA for use as a medicament.

In an alternative embodiment the invention provides a nucleotide construct such as anti-sense RNA, shRNA or miRNA for the manufacture of a medicament for the treatment of cancerous cell growth.

In an alternate embodiment the invention provides a small molecule or protein which interacts with or binds with a protein expressed by an abnormally spliced mRNA for the manufacture of a medicament for the treatment of cancerous cell growth.

The invention also provides a pharmaceutical composition comprising a nucleotide construct such as anti-sense RNA, shRNA or miRNA and a pharmaceutically acceptable diluent or carrier.

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In an alternate embodiment the invention provides a small molecule or protein which interacts with or binds with a protein expressed by an abnormally spliced mRNA and a pharmaceutically acceptable diluent or carrier.

Detailed Description of the Invention

The present invention will now be described by way of example only and with reference to the following diagrams;

5 Figure 1

Sequence alignments of human Bcl-2 splice variants in colorectal cell lines (including LoVo; SW48 and HCT116). Boxed areas indicate functional domains of Bcl-2. Note that Bcl-2 α -591 and Bcl-2 β -489 retain all functional domain sequences. Dashes indicate missing sequences from abnormally spliced Bcl-2 variants.

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Figure 2

Sizing of Bcl-2 genomic DNA following PCR amplification from individual human colorectal cell lines as indicated, using primers designed to span all abnormal splice sites identified to date. The predicted size for the intact genomic Bcl-2 DNA PCR-generated sequence, using the chosen primers, is 570 base pairs. This is the size observed in all colorectal cell lines tested to date, as indicated on the gels. [Note that genomic Bcl-2 is normally only spliced to generate the Bcl-2 α and Bcl-2 β variants].

Figure 3

Expression of abnormal alternatively spliced variants of human Bcl-2 in vitro and immunoprecipitation with anti-Bcl-2 antibodies. Bcl-2 mRNA from human colorectal cancer cells was reverse transcribed to produce a cDNA template from which cRNA was transcribed and translated. Translation was performed in the presence of 35S-methionine and radiolabelled protein was visualised by autoradiography following

immunoprecipitation and resolution by SDS-PAGE. Three abnormal splice variants are shown (Bcl- 2α -591; Bcl- 2β -489; and Bcl- 2β -420 as indicated).

Cloning and expression of abnormal alternative splice variants of Bcl-2 in vitro.

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Abnormal alternative splice variants of Bcl-2 mRNAs have been cloned from colorectal cancer cells and expressed in vitro. The results demonstrate that the abnormal alternative spliced variants of Bcl-2 are expressed as protein (Figure 3).

Lack of specific Bcl-2 epitopes was observed for the protein products encoded by the abnormal alternatively spliced Bcl-2 variants. Abnormal splicing in some way interferes with epitope availability for antibody recognition. It is proposed that epitope loss may prove to be a useful indicator of alternatively spliced Bcl-2 expression. For example, the variant Bcl- 2α -591 contains a novel splice junction between nucleotides 111 and 241 (Figure 1): the protein expressed endogenously from this splice variant in human cells reacts poorly with the N19 anti-Bcl-2 antibody in immunoblots (Jiang and Milner, 2003), and in immunoprecipitation reactions following its expression in vitro (Figure 3). Loss of antibody reactivity may also be evident in tissue sections stained by immunocytochemistry. Epitope loss or modification may prove to be of clinical and diagnostic importance for identifying the expression of abnormal alternative spliced variants of Bcl-2 in human tissues. The same prinicples apply to tissues of other mammalian species.

Alternative abnormal spliced variants of Bcl-2 may represent a tumour-related abnormality. This abnormality may not be restricted to cancers arising from

colorectal epithelial cells. Other tumour types may also be affected, including other epithelial tumours and/or tumours/malignancies arising from other cell types. Any tumour-related abnormality represents a promising target for selective therapy designed to selectively target malignancies in humans and in other mammalian species. Such therapies may, in principle, be designed to suppress gene expression using, for example, RNA interference. An alternative approach would be to target functional protein-protein interactions by, for example, small molecules designed to disrupt essential molecular interfaces between the Bcl-2 protein and its functional protein partners. Any differences in protein structure created as a result of abnormal alternative splicing of Bcl-2 mRNA represent potential tumour-specific targets for novel anti-cancer molecules and/or other reagents.

References:

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Jiang M & Milner J. Bcl-2 constitutively suppresses p53-dependent apoptosis
 in colorectal cancer cells. Genes & Development, 17; 832-837 (2003).

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Bcl-2a	atg	gcg	cac	qct	ggg	aga	aca	aaa	tac	ga <u>t</u>	aac	caa	gag	252	ata	ato	220	tac	ato	ast		226		-		1 25
Bcl-2a-591	atg	gcg	cac	qct	999	aga	aca	aaa	tac	gat	aac	caa	242	212	ata	atg	223	tac	atc	cat	tat	aay	ata	teg	cag	75
Bc1-2a-588	atg	gcg	cac	qct	ada	aga	aca	aaa	tac	gat	220	CGG	242	ata	ata	atg	220	tac	250	cat	-at	aay	aba	teg	cay	
Bc1-2a-480	atg	aca	cac	act	aga	aga	aca	223	tac	gat	220	-33	242	2+2	949	atg	229	tac	200	cat	Lat	aay	ctg	teg	cag	75
Bcl-2a-633	atg	aca	cac	act	aga	202	202	222	tac	900	226	-99	949	ata	919	atg	aay	Lac	acc	cat	cac	aag	ceg	reg	cag	75
Bcl-2β	ato	aca	Cac	act	222	272	200	333	tac	gat	aac		gag	aca	grg	atg	aag	tac	atc	cat	tat	aag	ctg	tcg	cag	75
Bcl 2B 489	ato	2-2	cac	act	222	200	202	999	tac	gac	aac		gag	aca	grg	atg	aag	cac	acc	cat	tat	aag	ctg	tcg	cag	75
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Bc1-2β-420	aro	2-2	Cac	get	222	aya	acg	999	cac	gac	aac	cgg	gag	ata	gtg	atg	aag	tac	atc	cat	tat	aag	ctg	tcg	cag	75
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Bcl-2a	agg	ggc	tac	gag	tgg	qat	aca	gga	gat	gtg	aar	acc	aca	ccc	cca	aaa	acc	900		~~~		~~~	260		+	150
Bcl-2a-591	agg	ggc	tac	gag	tgg	gat	aca	gga	gat	gtg	220	acc	5-5			399	900	900		gcg	ccg	gge	acc		CCC	130
Bc1-2a-588	agg	ggc	tac	gag	taa	gat	aca	gga	gat	gtg	220	300														111
Bc1-2a-480	agg	ggc	tac								350															
Bc1-2a-633	agg	qqc	qcq	aca	ata	atc	gag	acc	aga	acg	acc	+++	CCS	200	~~~	~~~										84
Bc1-2β	agg	ggc	tac	gag	taa	pat	aca	gga	gat	ata	900	~~~	cca	<u> </u>	909	909	909	909	966	aca	aca	gec	acg	aca	gtt	_150
Bc1-2β-489	agg	aac	tac	gag	taa	bat	2-2	224	ant	gtg	330	900	909	CCC	ccg	999	gee	gee	ccc	gca	ccg	ggc	atc	CCC	ECC	150
Bcl-2B-474	agg	ggc	cac	gag	taa	bat	2,2	224	gat nat	gtg	990	gcc														111
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Bcl -28-315	agg		-	· - -																						
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Bcl-2a	tcg	cag	ccc	999	cac	acg	CCC	cat	aca	gcc	qca	tcc	cqq	qac	cca	atc	acc	agg	acc	tca	CCG	cta	cao	acc	cca	225
Bc1-2α-591																										111
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Bcl-2a-480																										
Bcl-2a-633	acg	gcg																								156
Bc1-2β	tc <u>c</u>	cag	ccc	ggg	cac	acg	CCC	cat	cca	gcc	gca	tcc	cgc	gac	ccq	atc	qcc	agg	acc	t.ca	cca	cta	cac	acc	cca	180
Bc1-2β-489																										111
Bcl ·2β-474																										120
Bc1-2β-420																										69
Bcl-2β-315																										
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						gcc	gcg	999	cct	gcg	ctc	agc	ccg	gtg	cca	cct	gtg	gtc	cac	ctg	acc	ctc	cgc	cag	gcc	171
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Bcl-2α-480 Bcl-2α-633																										84
Bc1-2β							gcg	999	cct	gcg	ctc	agc	ccg	gtg	cca	cct	gtg	gtc	cac	ctg	acc	ctc	cgc	cag	gcc	213
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           tgg atg act gag tac ctg aac cgg cac ctg cac tgg atc cag gat aac gga ggc tgg --- --- 585
Bcl-2α-591 tgg atg act gag tac ctg aac cgg cac ctg cac tgg atc cag gat aac gga ggc tgg --- --- 456
Bcl-2α-588 tgg atg act gag tac ctg aac cgg cac ctg cac tgg atc cag gat aac gga ggc tgg --- --- 453
           tgg atg act gag tac ctg aac cgg cac ctg cac tgg atc cag gat aac gga ggc tgg --- --- --- 345
Bcl-2α-480
Bcl-2α-633 tgg atg act gag tac ctg aac cgg cac ctg cac tgg atc cag gat aac gga ggc tgg --- --- 498
           tgg atg act gag tac ctg aac cgg cac ctg cac tgg atc cag gat aac gga ggc tgg gta ggt gca tct ggt 600
Bcl-2β-489 tgg atg act gag tac ctg aac cgg cac ctg cac tgg atc cag gat aac gga ggc tgg gta ggt gca tct ggt 471
Bcl-2β-474 tgg atg act gag tac ctg aac cgg cac ctg cac tgg atc cag gat aac gga ggc tgg gta ggt gca tct ggt 456
Bcl-2β-420 tgg atg act gag tac ctg aac cgg cac ctg cac tgg atc cag gat aac gga ggc tgg gta ggt gca tet ggt 402
Bcl-2β-315 tgg atg act gag tac ctg aac cgg cac ctg cac tgg atc cag gat aac gga ggc tgg gta ggt gca tct ggt 297
           gat gcc ttt gtg gaa ctg tac ggc ccc agc atg cgg cct ctg ttt gat ttc tcc tgg 642
Bcl-2α-591 --- --- gat gcc ttt gtg gaa ctg tac ggc ccc agc atg cgg cct ctg ttt gat ttc tcc tgg 513
Bcl-2α-588 --- --- cet gat gcc ttt gtg gaa etg tac ggc ccc agc atg cgg cct ctg ttt gat ttc tcc tgg 510
Bcl-2α-480 --- --- gat gcc ttt gtg gaa ctg tac ggc ccc agc atg cgg cct ctg ttt gat ttc tcc tgg 402
Bcl-2α-633 --- --- gat gcc ttt gtg gaa ctg tac ggc ccc agc atg cgg cct ctg ttt gat ttc tcc tgg 555
           gat gtg agt ctg ggc tga 618
Bcl 2β 489 gat gtg agt ctg ggc tga 489
Bcl-2\beta-474 gat gtg agt ctg ggc tga 474
Bcl-2\beta-420 gat gtg agt ctg ggc tga 420
Bcl-2\beta-315 gat gtg agt ctg ggc tga 315
           ctg tet ctg aag act ctg ctc agt ttg gcc ctg gtg gga get tgc atc acc ctg ggt gcc tat ctg ggc cac aag 717
Bcl-2α
Bcl-2α-591 ctg tct ctg aag act ctg ctc agt ttg gcc ctg gtg gga gct tgc atc acc ctg ggt gcc tat ctg ggc cac aag 588
Bcl-2α-588 ctg tct ctg aag act ctg ctc agt ttg gcc ctg gtg gga gct tgc atc acc ctg ggt gcc tat ctg ggc cac aag 585
Bcl-2α-480 ctg tct ctg aag act ctg ctc agt ttg gcc ctg gtg gga gct tgc atc acc ctg ggt gcc tat ctg ggc cac aag 477
Bcl-2α-633 ctg tct ctg aag act ctg ctc agt ttg gcc ctg gtg gga gct tgc atc acc ctg ggt gcc tat ctg ggc cac aag 630
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Bcl-2α tga 720
Bcl-2α-591 tga 591
Bcl-2α-588 tga 588
Bcl-2α-480 tga 480
Bcl-2α-633 tga 633
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